

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 17, 2003, 16:09:08 ; Search time 32 Seconds
(without alignments)
1558.231 Million cell updates/sec

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Title:      US-09-978-309A-74
Perfect score: 1195
Sequence:    1 QEKYDSMWQSLSDVTAQES.....KKQSETKQLELNKYLGIK 2422

```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post processing:
Minimum match 08
Maximum Match 1008
Listing first 45 summaries

```

1:  sp.archaea:*
2:  sp.bacteria:*
3:  sp.fungi:*
4:  sp.human:*
5:  sp.invertebrate:*
6:  sp.mammal:*
7:  sp.minc:*
8:  sp.ornelle:*
9:  sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vetehrable:*
14: sp.unclassified:*
15: sp.vyrus:*
16: sp.bacteriap:*
17: sp.archaeap:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB	ID	Description
1	917	76.7	836	11	08VD22	08vd12 mus musculus
2	905.5	75.8	476	11	092026	092026 mus sp. hya
3	893	74.7	713	11	09W07	09w17 rattus norv
4	338	28.3	82	6	09SUG7	09s197 ovis aries
5	338	28.3	82	6	08SPM2	08spm2 bos taurus
6	209	17.5	436	4	096JX7	096jx7 homo sapien
7	209	17.5	1388	4	09MS87	09ms87 homo sapien
8	193.5	16.2	1944	13	09DGS5	09dgs5 gallus galli
9	193	16.2	1388	13	091785	091785 xenopus lae
10	191	16.0	795	4	09H2G7	09h2g7 homo sapien
11	181	16.0	804	4	087C31	08tc31 homo sapien
12	191	16.0	1410	4	014J21	014j21 homo sapien
13	191	16.0	1411	4	015075	015075 homo sapien
14	190	15.9	1699	5	044929	044929 drosophila
15	189.5	15.9	1941	13	09DGS4	09dgm4 gallus galli
16	189	15.8	1690	5	09VJES	09vjes drosophila

17	187	15.6	826	13	Q9YHD5	Q9Yhb5 rana calesab
18	185.5	15.5	1790	3	Q07380	Q07380 saccharomyc
19	183.5	15.4	1937	6	Q9TV62	Q9TV62 sus scrofa
20	182.5	15.3	1929	13	Q98T06	Q98T06 notochientia
21	182.5	15.3	1935	13	Q90ZE5	Q90ZE5 brachydanila
22	182.5	15.3	1940	6	Q9BE41	Q9BE41 bos taurus
23	181.5	15.2	1958	11	Q92ZD2	Q92ZD2 mus musculu
24	180.5	15.1	1938	6	Q9BE40	Q9BE40 bos taurus
25	179.5	15.0	1939	13	Q9PVT2	Q9PVT2 gallus galli
26	179	15.0	1463	5	Q9GTZ0	Q9GTZ0 strongyloce
27	178.5	14.9	632	5	Q967Z0	Q967Z0 dermatophog
28	178.5	14.9	1930	13	Q9DGD5	Q9DGD5 pennaria ari
29	178.5	14.9	1939	6	Q9TV61	Q9TV61 sus scrofa
30	178	14.9	609	17	Q98TX4	Q98TX4 methanopyru
31	176.5	14.8	975	13	Q98TQ3	Q98TQ3 notochientia
32	176.5	14.8	1939	6	Q9TV63	Q9TV63 sus scrofa
33	175.5	14.7	746	4	Q9H6N6	Q9H6N6 homo sapien
34	175.5	14.7	1945	6	Q97757	Q97757 felis silve
35	174.5	14.6	1936	13	Q90VE6	Q90VE6 paracitribili
36	174	14.6	549	5	Q9XZV8	Q9XZV8 hydra atten
37	171	14.3	1320	11	Q9JK25	Q9JK25 ratu
38	170.5	14.3	1119	13	P87344	P87344 thelagra chi
39	170	14.2	1388	11	P70336	P70336 mus musculu
40	169.5	14.2	1938	13	Q9IBD7	Q9IBD7 seriola dum
41	169	14.1	764	13	Q91411	Q91411 gallus galli
42	169	14.1	792	11	Q9JHZ3	Q9JHZ3 ratu
43	169	14.1	806	11	Q9VD04	Q9VD04 mus musculu
44	169	14.1	837	11	Q9JHZ4	Q9JHZ4 ratu
45	169	14.1	1469	5	Q8T805	Q8T805 dtrosophila

ALIGNMENTS

ID	Q8VDR2	PRELIMINARY:	PRT:	836 AA.
Q8VDR2	Q8VDR2			
DT	01-MAR-2002 (TREMBLrel. 20, Created)			
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	Similar to hyaluronan mediated motility receptor (RHAMM).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Strausberg R.;			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC021427; AAH21427.1; -			
KW	Receptor.			
SO	SEQUENCE			
	836 AA; 96670 MW; B9BDNA22EBE6A652 CRC64;			
	Query Match	76.7%;	Score 917;	DB 11; Length 836;
	Best Local Similarity	76.4%;	Pred. NO. 1.5e-38;	
	Matches 185; Conservative 19; Mismatches 38; Indels 0; Gaps 0			
QY	1 QEKYDSWQSLIEDYTAQFESYKALTLASEFDKLTENSSLOEKAAGAKNAEYHOIILAT 60			
Db	568 QEKINDTRAQSLRDVTAQLESTKSSLTLEKIEDKLENTLTLOEKVAAAEKSEVVDQOILTA 627			
QY	61 ESSNOEYVRMLDLDTQTSALKETETKEITVFSLOKITPDLONLQOEEDFRKQLEDEGR 120			
Db	628 ESTNOGEVAVRWQDLONRSTLKEEETKETSSTLEKTPDLOKNGLRQDDEDFRKQLEBKGR 687			
QY	121 KAEKENTTAELTEEINKWRLLYEELYNKTRKPFQIOLDAFEWEKQALLNEHGAQOELNKI 180			
Db	688 TAEKENVTETLTMETINKWRLLYEELYEXTKPFQOQDLDAFEAKQALLNEHGAQTOEOLNKI 747			
QY	181 RDSYAKLLGHONLKOKIKHYVVKLDENSQKLSEVSKLCKQLAKKQKQSETKQLOEELNKYL 240			
Db	748 RDSYAKLLGHONLKOKIKHYVVKLDENSQKLSEVSKLCKQLAKKQKQSETKQLOEELNKYL 807			

OY 241 IK 242
DB 808 IR 809

RESULT 2

OY 092026 PRELIMINARY; PRT: 476 AA.
AC 092026;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE Hyaluronan receptor.
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92299690; PubMed=1376732;
RA Hardwick C., Hoare K., Owens R., Hohn H.P., Hook M., Moore D.,
RA Cripps V., Austen L., Nance D.M., Turley E.A.;
RT "Molecular cloning of a novel hyaluronan receptor that mediates tumor
cell motility.";
RL J. Cell Biol. 117:1343-1350(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92348516; PubMed=1639856;
RA Hardwick C., Hoare K., Owens R., Hohn H.P., Hook M., Moore D.,
RA Cripps V., Austen L., Nance D.M., Turley E.A.;
RT "Correction. Molecular cloning of a novel hyaluronan receptor that
mediates tumor cell motility.";
RL J. Cell Biol. 118:753-753(1992).
DR EMBL: S41029; AAA09809.1;
KW Receptor.
SQ SEQUENCE 476 AA; 55486 MW; 62DCA82045EE0CB2 CRC64;

Query Match 75.8%; Score 905.5; DB 11; Length 476;
Best Local Similarity 76.0%; Pred. No. 3, 2e-38;
Matches 184; Conservative 20; Mismatches 37; Indels 1; Gaps 1;

OY 1 QEKYDSWVOSLEEDVTAQFESYKALTAASEIDKLENSLOEKAKAKNAEDVOHOTLAT 60
DB 209 QEKYDNTAQSLRVSQLESYKSTLKEIDKLENTLLOEKYAMAEKESVEDVQOQILTA 268
OY 61 ESSNOEYVRMLDLQTSALKEITEIKETVPSFOKITDLONOLOKQOEDPRKOLEDEGR 120
DB 269 ESTNOEYARVQDLONRSTLKEIEIKETTSFLEKITDLONOLOKQOEDPRKOLEDEGR 328
OY 121 KAKEKNTALTEIKKRWLLYEELYNKTRPFOIOLDAFEVEKQALLNEHGAQOELNKT 180
DB 329 TKEKEVMTLEIMEIKRWLLYEELYNKTRPFOIOLDAFEVEKQALLNEHGAQOELNKT 387
OY 181 RDSYAKLLGHONLKQIKKHVVKLDKNSQKSEVSKLRQALKKQSEKTKLOEELNKVYG 240
DB 388 RDSYAKLLGHONLKQIKKHVVKLDKNSQKSEVSKLRQALKKQSEKTKLOEELNKVYG 447
OY 241 IK 242
DB 448 IR 449

RESULT 3

OY 09WU77 PRELIMINARY; PRT: 713 AA.
AC 09WU77;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DE Hyaluronan receptor RHAMM.
GN RHAMM.
OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY;
RA Li X., Lynn B., Nagy J.L., Cattini P.A.;
RT "RHAMM CDNA from rat brain.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PHOCHROMOCYTOMA;
RA Lynn B.D., Li X., Cattini P.A., Nagy J.L.;
RT "Sequence, protein expression and erk association of the hyaladherin
RHAMM in PC12 cells.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF133037; AAD24473.1;
DR EMBL: AF336825; AAK21904.1;
KW Receptor.
SQ SEQUENCE 713 AA; 82395 MW; 2PE310D57596CB3 CRC64;

Query Match 74.7%; Score 893; DB 11; Length 713;
Best Local Similarity 74.0%; Pred. No. 2e-37;
Matches 179; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

OY 1 QEKYDSWVOSLEEDVTAQFESYKALTAASEIDKLENSLOEKAKAKNAEDVOHOTLAT 60
DB 442 QEKSDPAQTLRVTQALLESYKSTLKEIDKLENTLLOEKYAMAEKESVEDVQOQILTA 501
OY 61 ESSNOEYVRMLDLQTSALKEITEIKETVPSFOKITDLONOLOKQOEDPRKOLEDEGR 120
DB 502 ESTNOEYARVQDLONRSTLKEIEIKETTSFLEKITDLONOLOKQOEDPRKOLEDEGR 561
OY 121 KAKEKNTALTEIKKRWLLYEELYNKTRPFOIOLDAFEVEKQALLNEHGAQOELNKT 180
DB 562 MTKETAVVTEIMEIKRWLLYEELYNKTRPFOIOLDAFEVEKQALLNEHGAQOELNKT 621
OY 181 RDSYAKLLGHONLKQIKKHVVKLDKNSQKSEVSKLRQALKKQSEKTKLOEELNKVYG 240
DB 622 RDSYAKLLGHONLKQIKKHVVKLDKNSQKSEVSKLRQALKKQSEKTKLOEELNKVYG 681
OY 241 IK 242
DB 682 IR 683

RESULT 4

OY 095JG7 PRELIMINARY; PRT: 82 AA.
AC 095JG7;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE Hyaluronan acid-mediated motility receptor (Fragmant).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TRACHEA;
RA Aoki T.A., Forteza R.M., Conner G.E.;
RT "Receptor for hyaluronan acid mediated motility in sheep (Ovis aries)
trachea.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF10973; AAK69578.1;
KW Receptor.
FT NON_TER.
SQ SEQUENCE 82 AA; 9452 MW; 46B87555C0F1B66 CRC64;

Query Match 28.3%; Score 338; DB 6; Length 82;

Best Local Similarity 89.5%; Pred. No. 1.3e-10;
Matches 68; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 167 LNEHGAQEOQLNKIRDSYAKLLGHONLKOKIKHYVVKLDKNSOLKSEVSKLRQOLAKKKO 226

DB 1 LNEHGAQEOQLNKIRDSYAKLLGHONLKOKIKHYVVKLDKNSOLKSEVSKLRQOLAKKKO 60

QY 227 SETKLOEELNKVLGIR 242
DB 61 SEAKLOEELNKVLGIR 76

RESULT 5

OSPM2 PRELIMINARY; PRT; 82 AA.

DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE Receptor for hyaluronidic acid mediated motility (Fragment).
GN RHAMM.

OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovine; Bos.
OX NCBI_TaxID=9913;

RN 11
RP SEQUENCE FROM N.A.

RC TISSUE-Ovary;

RA Schoenfelder M., Einspanier R.;

RT "Expression of HAS-system during oocyte maturation in the cow."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; A439694; CAD29126.1;

FT NON_TER 1 1

SO SEQUENCE 82 AA; 9452 MW; 46B87555C0F1B66 CRC64;

Query Match 28.3%; Score 338; DB 6; Length 82;
Best Local Similarity 89.5%; Pred. No. 1.3e-10;

Matches 68; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 167 LNEHGAQEOQLNKIRDSYAKLLGHONLKOKIKHYVVKLDKNSOLKSEVSKLRQOLAKKKO 226

DB 1 LNEHGAQEOQLNKIRDSYAKLLGHONLKOKIKHYVVKLDKNSOLKSEVSKLRQOLAKKKO 60

QY 227 SETKLOEELNKVLGIR 242

DB 61 SEAKLOEELNKVLGIR 76

RESULT 6

Q96JX7 PRELIMINARY; PRT; 436 AA.

AC 096JX7; 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DE CDNA FLJ14910 f1s, clone PLACE1006368, weakly similar to

DE hyaluronan-mediated motility receptor.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN 11
RP SEQUENCE FROM N.A.

RC TISSUE-PLACENTA;

RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Takiguchi S.,

RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y.,

RA Niimiya K., Iwayanagi T.;

RT "NEDO human cDNA sequencing project."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK027816; BAB55389.1;

SO SEQUENCE 436 AA; 51433 MW; 3BE3ABDB7A7821D CRC64;

Query Match 17.5%; Score 209; DB 4; Length 436;
Best Local Similarity 24.8%; Pred. No. 0.0018;

Matches 68; Conservative 57; Mismatches 101; Indels 48; Gaps 7;

QY 1 QEKYDSMVOSLEDV-----TAOFESKA---LTASEIDKLKNSLOEKA 43

DB 166 KNEYNFKMROLEHVMSAADPOSPKTPPHQTHLAKLTOTBOEDIEDGRASSTSEHLV 225

QY 44 AKAGNAEDVOHOLATSESSNOEYVRLDLO---TSALKETEIKETVSPLOKTDLO 100

DB 226 TKLNEDDEVKNAELRKEDLRKEMENIRLESQOLIEKNMLLOGLDDIK---RQKENSQ 282

QY 101 N-----OLKQOEDFRKO-----LEDEGRKAKEKNTVAELTEINKV 138

DB 283 NHPDNOOLKNEQESIKERLAKSKIYEMLKMKADLEEVQSAlyNKMECLMTDEVERT 342

QY 139 RLIEELYNKTRFQLOLAFVEYEQALLNEHGAQEOQLNKIRDSYAKLLGHONLKOKIK 198

DB 343 QTLSEKAFQEKEDLRSLKEMYEERERTSQEMELRKQYECIAENGKLIHGHLQKIQ 402

QY 199 HVKLKDENSOLKSEVSKLRQO---LAKKQSEF 229

DB 403 YVRLKKNVRLAEETEKRLAENVFLKERRSES 436

RESULT 7

Q9NS87 PRELIMINARY; PRT; 1388 AA.

AC 09NS87; 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DE Kinesin-like protein 2.

GN HKLP2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN 11
RP SEQUENCE FROM N.A.

RA MEDLINE-20435852; PubMed-10878014;

RA Suetshi M., Takagi M., Yoneda Y.;

RT "The Forkhead-associated Domain of Ki-67 Antigen Interacts with the

RT Novel Kinesin-like Protein HKLP2."

RL J. Biol. Chem. 275:28888-28892(2000).

DR EMBL; AB035898; BAB03309.1;

DR HSP; P17119; 3KAR.

DR InterPro: IPR001752; kinesin_motor.

DR Pfam: PF00225; kinesin; 1.

DR PRINTS: PRO0380; KINESINHEAVY.

DR SMART: SM00129; KISC; 1.

DR PROSITE: PS50067; KINESIN_MOTOR_DOMAIN2; 1.

KW ATP-binding; Coiled coil; Microtubules; Motor protein.

SO SEQUENCE 1388 AA; 160160 MW; E127EB4B991CA83A CRC64;

Query Match 17.5%; Score 209; DB 4; Length 1388;
Best Local Similarity 24.8%; Pred. No. 0.0053;

Matches 68; Conservative 57; Mismatches 101; Indels 48; Gaps 7;

QY 1 QEKYDSMVOSLEDV-----TAOFESKA---LTASEIDKLKNSLOEKA 43

DB 1118 KNEYNFKMROLEHVMSAADPOSPKTPPHQTHLAKLTOTBOEDIEDGRASSTSEHLV 1177

QY 44 AKAGNAEDVOHOLATSESSNOEYVRLDLO---TSALKETEIKETVSPLOKTDLO 100

DB 1178 TKLNEDDEVKNAELRKEDLRKEMENIRLESQOLIEKNMLLOGLDDIK---RQKENSQ 1234

QY 101 N-----OLKQOEDFRKO-----LEDEGRKAKEKNTVAELTEINKV 138

Db 1235 NHPDNOQLKNEDEESIKERLAKSKIYEELKAKADLEFEVQSLYNKECECLRMTEVEERT 1294
 QY 139 RLLYEELYNKTPFOIQLDAFEVEKQALLNEHGAQEOQLNIRDSYAKLLGHONLKOK 198
 Db 1295 QLESKAPQEKQESKLEEMEYEEERPTSOEEMELRKQVECLAENGKLVGNONLHOKIO 1354
 QY 199 HVVKLKDENSOLKSSEVSKLRQ---LAKKQOSET 229
 Db 1355 YVVRLLKENVRKLAETEKIRANVFLKKEKRSSES 1388

RESULT 8

Q9DGM5 PRELIMINARY: PRT: 1944 AA.
 ID 09DGM5:
 AC 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Q., Bandman E.
 RT "Seven skeletal myosin heavy chain genes (MYHC) are organized as a
 multi-gene complex in the chicken genome."
 RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF272033; AAF99314.1;
 DR HSSP: P13538; 2MYS.
 DR InterPro: IPR000048; 10_region.
 DR InterPro: IPR001609; myosin_head.
 DR InterPro: IPR004099; myosin_N.
 DR InterPro: IPR002928; myosin_tail.
 DR InterPro: IPR000533; Tropomyosin.
 DR Pfam: PF00612; IQ: 1.
 DR Pfam: PF00063; myosin_head: 1.
 DR Pfam: PF02736; myosin_N: 1.
 DR Pfam: PF01576; myosin_tail: 1.
 DR PRINTS: PRO0193; MYOSINHEAVY.
 DR PRINTS: PRO0194; TROPOMYOSIN.
 DR ProDom: PD000355; myosin_head: 1.
 DR SMART: SM00015; IQ: 1.
 DR SMART: SM00242; MYSC: 1.
 SO SEQUENCE 1944 AA; 223211 MW; 154F438220072D68 CRC64;

Query Match 16.2%; Score 193.5; DB 13; Length 1944;
 Best Local Similarity 21.3%; Pred. No. 0.044;

Matches 76; Conservative 53; Mismatches 106; Indels 121; Gaps 9;

QY 8 VQSLQEDVTAQFESYKALTASEIEDLKLENSLQEKRAAKGNAEDVOHILATESNOEY 67
 Db 1215 IONLQVQKQLEKESSELMETIDDLASNMESVSKANLEKCRLEEDLSIKTSKEEBH 1274
 QY 68 VMMLIDLQTSALKTELEKEIT-----VSFLQITDLOQLKOO----- 106
 Db 1275 QRMINDLSTQRRARLQTESGEYSROYEEKDALISQSRGQATQOIEELKRLHEEIRAK 1334
 QY 107 -----EED-----FKQLEDEGKRAKENTTAELTEINKWRLY-----DEL 145
 Db 1335 NALAHALQSANRHDCLLREYQEEQEAQGELOFALSKANSSEVAQWRKYETDAIQRTBEL 1394
 QY 146 YNKTQFQIOLD-----AFVEKQALLNE-----HGAQEOQLNIR 181
 Db 1395 EEAKKKLAQRLODAEHEVEAVNACASLEKTKQRLQNEVEDLMDVERANACARLDKQ 1454
 QY 182 DSYAKLLGHONLK-----OKIKVVLKQENSOLOK 211
 Db 1455 KNPFKIIAEMWQKEETOAELEASQKESRSSTELFKKKNAYEESLDHLETLTKRENKNO 1514

QY 212 SEVSKLRQALK-----KKO-----SETKQEOELNVLGK 242
 Db 1515 QEISDLTQIAGGGAHIELEKVKQKQIDQEKSEIOALEEASLEHEGKRLIQ 1570

RESULT 9

Q91785 PRELIMINARY: PRT: 1388 AA.
 ID 091785:
 AC 091785:
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 OS KLP2 protein.
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bolet H., Karsenti E., Vernos I.
 RT "Xlp2, a new Xenopus centrosomal kinesin-like protein required for
 centrosome separation during mitosis."
 RL Cell 0:0-0(0).
 DR EMBL: X94082; CAA63826.1;
 DR HSSP: P17119; 3KAR.
 DR InterPro: IPR001752; kinesin_motor.
 DR Pfam: PF00225; kinesin; 1.
 DR PRINTS: PRO0380; KINESINHEAVY.
 DR SMART: SM00129; KISC: 1.
 DR PROSITE: PS00411; KINESIN_MOTOR_DOMAIN1; 1.
 DR PROSITE: PS50667; KINESIN_MOTOR_DOMAIN2; 1.
 KW ATP-binding; Coiled coil; Microtubules; Motor protein.
 SO SEQUENCE 1388 AA; 159141 MW; 1F882538B9AE28E CRC64;

Query Match 16.2%; Score 193; DB 13; Length 1388;
 Best Local Similarity 22.9%; Pred. No. 0.034;

Matches 71; Conservative 51; Mismatches 92; Indels 96; Gaps 7;

QY 9 QSLQEDVTAQFESYKALTASEIEDL-----KLENSLQEKRAAKGNA 50
 Db 1079 EELEKLTFAFNQEOALHTHEKEIYEKEQOISELTNQVYKLTMDLEISRQEKIRASNS 1138
 QY 51 -----EDVQOILATE-----SSNOEYVMMLIDLQTK 77
 Db 1139 SSPVVLPEPTPEPGNPYDSEIANQKRNLTLEILVSEINERTSKNEEIRL-----K 1192
 QY 78 SALKTELEKEITVSFLQRT-IDLOQLK-----QOEDEPRKQLEDEGKRA 122
 Db 1193 MQLCETEMRLQIONLQCMCKELKSQLENCNNVYKMSDQKPSMDQDLKRELEKESVSRM 1252
 QY 123 EKENTTA-----ELTEINKWRLYEELYNKTPFOIQLDA 158
 Db 1253 EKGRATEIILQLQELQELTNRILCTKQSHLSLELSKETERTSLAKAFTEKEEIRSLIEG 1312
 QY 159 FEVEKQALLNBEHGAQEOQLNIRDSYAKLLGHONLKQIKRVVLKQENSOLOKSEVSKLR 218
 Db 1313 KYEETEKLSHLDMLRKQVLEFLAENGKLLGHONPNQKIOYLVALKKENNALLEAEKLR 1372
 QY 219 QQLAKKQOSET 228
 Db 1373 IENFLKESK 1382

RESULT 10

Q9H2G7 PRELIMINARY: PRT: 795 AA.
 ID 09H2G7:
 AC 09H2G7:
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 SO CTL tumor antigen set-1 (Fragment).

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=21143360; PubMed=11149944;
RA Eichmüller S., Usener D., Dummer R., Stein A., Thiel D.,
RA Schandorf D.,
RT "Serological detection of cutaneous T-cell lymphoma-associated
RT antigens."
RL Proc. Natl. Acad. Sci. U.S.A. 98:629-634(2001).
DR EMBL: AF273043; AAC34903.1; -.
FT NON_TER
SQ SEQUENCE 795 AA; 93500 MW; 45472A86A5A7ADFA CRC64;

Query Match 16.0%; Score 191; DB 4; Length 795;
Best Local Similarity 23.3%; Pred. No. 0.025;
Matches 79; Conservative 53; Mismatches 103; Indels 104; Gaps 12;

QY 1 OEKYDSMVOSLEDVTAOFESYKALPTAS---EIEDLK-----LENSLQEKAAKAG 47
DB 402 EDQKILTMELQKSSLEEMTKLTNNKEVELELKVGEKFTLYENKQF-EKTAEBL 460
QY 48 KNAE-----DVOHQIATESSNOEYVRMLDLOTK---SALKETEI---- 85
DB 461 KCTEOELIGLQAREKEVHDLFIQTAITTSSEQYSEKVEDLKTLEENKLTNLTSHC 520
QY 86 -----KETVSEFLQKIDLOLQKOEEDFKOLEDEGRAEAKENTTAELTEINIK 138
DB 521 NKLSLENKELT---OETSDMTLELNQOEDINNNKOEERMLKQIENLOETETOLRNEL 576
QY 139 RLVEELYNKTKPFOIQLDAFE-----VEQALLNEHGAQEOU 177
DB 577 EYVREELKQKRDVEVKCKLDKSEENCNLRKOVENKKYIEELQOEKKALKKGTASKOL 636
QY 178 N-----KIRDSYA-----KLGHONLKOKIKHVKLKDENSOLK 211
DB 637 NYVEIKVKNLELESASAKQFGEITPTQYKEIEDKQISENLELEVEKAKVIADENAVKIQ 696
QY 212 SEVSKLRQ-----LAKKQSETKLOEELNKVIGI 241
DB 697 KEIDK-RCQHKIAEMVAMEKHKHQYDKITIEERDSELGL 734

RESULT 11
O8RC31
ID O8TC31; PRELIMINARY; PRT; 804 AA.
AC O8TC31;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DR 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Similar to synaptonemal complex protein 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC026162; AAH26162.1; -.
FT NON_TER
SQ SEQUENCE 804 AA; 94504 MW; C7A6FAB55989CEA5 CRC64;

Query Match 16.0%; Score 191; DB 4; Length 804;
Best Local Similarity 23.3%; Pred. No. 0.025;
Matches 79; Conservative 53; Mismatches 103; Indels 104; Gaps 12;

QY 1 OEKYDSMVOSLEDVTAOFESYKALPTAS---EIEDLK-----LENSLQEKAAKAG 47
DB 402 EDQKILTMELQKSSLEEMTKLTNNKEVELELKVGEKFTLYENKQF-EKTAEBL 460

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QY 48 KNAE-----DVOHQIATESSNOEYVRMLDLOTK---SALKETEI---- 85
DB 461 KCTEOELIGLQAREKEVHDLFIQTAITTSSEQYSEKVEDLKTLEENKLTNLTSHC 520
QY 86 -----KETVSEFLQKIDLOLQKOEEDFKOLEDEGRAEAKENTTAELTEINIK 138
DB 521 NKLSLENKELT---OETSDMTLELNQOEDINNNKOEERMLKQIENLOETETOLRNEL 576
QY 139 RLVEELYNKTKPFOIQLDAFE-----VEQALLNEHGAQEOU 177
DB 577 EYVREELKQKRDVEVKCKLDKSEENCNLRKOVENKKYIEELQOEKKALKKGTASKOL 636
QY 178 N-----KIRDSYA-----KLGHONLKOKIKHVKLKDENSOLK 211
DB 637 NYVEIKVKNLELESASAKQFGEITPTQYKEIEDKQISENLELEVEKAKVIADENAVKIQ 696
QY 212 SEVSKLRQ-----LAKKQSETKLOEELNKVIGI 241
DB 697 KEIDK-RCQHKIAEMVAMEKHKHQYDKITIEERDSELGL 734

RESULT 12
O14221
ID O14221; PRELIMINARY; PRT; 1410 AA.
AC O14221;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DR 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Endosome-associated protein.
GN BEAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95286647; PubMed=7768953;
RA Mu F.T., Callaghan J.M., Steele-Mortimer O., Stenmark H., Patton R.G.,
RA Campbell P.L., McCluskey J., Yeo J.P., Tock E.P., Toh B.H.,
RT "EEA1, an early endosome-associated protein, EEA1 is a conserved
RT alpha-helical peripheral membrane protein flanked by cysteine
RT 'fingers' and contains a calmodulin-binding IQ motif."
RL J. Biol. Chem. 270:13503-13511(1995).
DR EMBL: LA0157; AAA79121.1; -.
DR InterPro: IPR000822; Znf_C2H2.
DR InterPro: IPR000306; Znf_FYVE.
DR Pfam: PF01363; FYVE; 1.
DR SMART: SM00064; FYVE; 1.
DR SMART: SM00355; Znf_C2H2; 1.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
DR PROSITE: PS00157; ZINC_FINGER_C2H2_2; 1.
FT NON_TER
SQ SEQUENCE 1410 AA; 162496 MW; DF0F9464D70A8AD CRC64;

Query Match 16.0%; Score 191; DB 4; Length 1410;
Best Local Similarity 27.7%; Pred. No. 0.043;
Matches 74; Conservative 50; Mismatches 69; Indels 74; Gaps 12;

QY 1 OEKYDSMVOSLEDVTAOFESYKALPTASIEDLKLENSLQEKAAKAGNAEDVOHQ----- 56
DB 715 KEVYLSLQKTELELQK-----KLNDSLEVYASKE-QALDDLOQROLN 760
QY 57 -----ILATESSNO-----EYVRML-LDLOTSALKETEKEITVSEFLQKIDLOLQK 106
DB 761 TDLELRATELSKQLEMEKEIVSTRDLQKKS-----EALIESIKKLT-----KOE 806
QY 107 EEDFKOLEDEGRAEAKENTTAELTEINIKRWLYEELYNKTKPFOIQLDAFEVKAL 166
DB 807 EE---KOLIKODEFLISOET-----KIOHEELNNIQTVTTELQKVKNEKAL 851
QY 167 LNEHGAQEOUINKTRDSY-----AKLGHONLKOKIKHVKLKDENSOLK 211

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Db 852 MTELSTVVKDLKSLVSDSLKNSKSEFEKNQKRAILDEKTEKELKHQLOVQMENT-LK 910
QY 212 SEVSKRLCOLAKKQSETKLOEELNKV 238
Db 911 -EOKELKSLKEKEKESHOLKLELNSM 936

RESULT 13

ID 015075 PRELIMINARY; PRT: 1411 AA.
AC 015075;
DT 01-NOV-1996 (TREMBLREL. 01, Created)
DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)
DE 01-MAR-2002 (TREMBLREL. 20, Last annotation update)
OS Endosomal protein.
GN P162.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN NCBI_TaxID=9606;
RX [1].
RP SEQUENCE FROM N.A.
RA Seelig H.P.;
RL Submitted (Apr-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: X78998; CA55632.1;
DR InterPro: IPR000822; Znf_C2H2.
DR InterPro: IPR000306; Znf_FYVE.
DR Pfam: PF01363; FYVE; 1.
DR SMART: SM00064; FYVE; 1.
DR SMART: SM00355; Znf_C2H2; 1.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 1.
DR DNA-binding; Zinc-finger.
SQ SEQUENCE 1411 AA; 162465 MW; C3B1777FE34B6BD CRC64;

Query Match 16.0%; Score 191; DB 4; Length 1411;
Best Local Similarity 27.7%; Pred. No. 0.043;
Matches 74; Conservative 50; Mismatches 69; Indels 74; Gaps 12;

QY 1 QERYDSKVSQLEDTVAQFESYKALTYSEIEDLKLENSLOEKAKGNADVOHO-----56
Db 715 KERYLSLEQTEELQIK-----KLEADSLVSKSK-QLAQDLOOQROLN 760
QY 57 -----ILATESNC-----EYRML-LDLOTKSLKETEKEITVSELOKTTDLONLQOO 106
Db 761 TDELFATLSTKOLEMEKEKIVSSTRDLQKKS-----EALSLKQKLT-----KE 806
QY 107 EEDFRQLEDESGRAKAKENTTALTEELNKMLLYEELYNKTKPQIQLODAFEVKKQL 166
Db 807 EE---KQILKQDPETLSQET-----KIQHEELNNRIQTTVTELQVKMEKEAL 851
QY 167 LNEHGAQOLNKIRDSY-----AKLIGHQNKOKIKHVYKLDKENSQK 211
Db 852 MTELSTVVKDLKSLVSDSLKNSKSEFEKNQKRAILDEKTEKELKHQLOVQMENT-LK 910
QY 212 SEVSKRLCOLAKKQSETKLOEELNKV 238
Db 911 -EOKELKSLKEKEKESHOLKLELNSM 936

RESULT 14

ID 044929 PRELIMINARY; PRT: 1690 AA.
AC 044929;
DT 01-JUN-1998 (TREMBLREL. 06, Created)
DT 01-JUN-1998 (TREMBLREL. 06, Last sequence update)
DE Microtubule binding protein D-CLIP-190.
GN CLIP-190 OR CG5020.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON R.
RA Lantz V.A., Miller K.G.;
RL J. Cell Biol. 0:0-0(1998).
DR EMBL: AF041382; AAB96783.1;
DR Flybase: FBgn020503; CLIP-190.
DR InterPro: IPR000938; CAP-Gly.
DR Pfam: PF01302; CAP_GLY; 2.
SQ SEQUENCE 1690 AA; 189103 MW; BE4F48FD15F17A7C CRC64;

Query Match 15.9%; Score 190; DB 5; Length 1690;
Best Local Similarity 27.1%; Pred. No. 0.057;
Matches 75; Conservative 53; Mismatches 107; Indels 42; Gaps 11;

QY 2 EKYSMVQSLQEDVTAQFESYKALTYSEIEDLKLENSLOEKRAA---KAGNAEDVOHQIL 58
Db 629 EQLRELQOLDEVTQOLNVOKKADSDLDMLRLQKEGTEKSTLLEKTELVQIKQAA 688
QY 59 ATSSNQEYRMLDLOTKSALKEITKEITVSELOK-----TDLONLQOOE-EDFR 111
Db 689 KTLQDKQOLKQISDLK-QLAEQEKLVREKTENAINQIQLEKESIEQOLALKQNELEDRQ 747
QY 112 KQLEDEGR---KAERNTTALTEERINKRWRLYEELYNKT---KPFQLODAFEVKKQ 164
Db 748 KQSESEVHLQELKQANTQKDELVESEGSGLKQLOOLEKTKLGHKTLQAALELKKKE 807
QY 165 ALNENGAQOL-NKIRDSYAKL---LGHONLKQKI-----KHVYKLDKENSQK 211
Db 808 TIKKEEQLQLOQSLKSAESALKVYQVQLQLOQAAASGEGSKTVAKLHDELQSLK 867
QY 212 SEVSKRLCOL-----AKKQSEK---KLOEELNK 237
Db 868 SQAEFTQSELKSTESNLKAKSKOLEANGLSLEBAKK 904

RESULT 15

ID 09DGM4 PRELIMINARY; PRT: 1941 AA.
AC 09DGM4;
DT 01-MAR-2001 (TREMBLREL. 16, Created)
DT 01-MAR-2001 (TREMBLREL. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLREL. 21, Last annotation update)
DE Fast myosin heavy chain-isoform 3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN NCBI_TaxID=9031;
RP SEQUENCE FROM N.A.
RA Zhang Q., Bandman E.;
RT "Seven skeletal myosin heavy chain genes (MyHC) are organized as a multigene complex in the chicken genome."
RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF272034; AAF9315.1;
DR HSSP: P13538; 2MYS.
DR InterPro: IPR000048; IQ_region.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; myosin_N.
DR InterPro: IPR002928; myosin_tail.
DR InterPro: IPR000533; Tropomyosin.
DR Pfam: PF00612; IQ; 2.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF02736; myosin_N; 1.
DR Pfam: PF01576; myosin_tail; 1.
DR PRINTS: PR00193; MYOSTINHEAVY.
DR PRINTS: PR00194; TROPOMYSIN.
DR PRODOM: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR SMART: SM00242; MYSC; 1.
SQ SEQUENCE 1941 AA; 223162 MW; 9C8597C1CFCFIDEC CRC64;

